

HG52.apr

Section 1						
	(1)	1	10	20	30	45
AAH18130_PAR1L	(1)	----	MRSPSAAWLLGAA	ILLAASLSCSGT	IQGTNRSSKGRSL	IG
NP_001983_PAR1	(1)	MGPRRLLLVAACF	SLCGPLLSARTR	ARRPESKATNAT	LDPRSFL	
NP_835230_P2Y8	(1)	-----				
TransBD243560_HG52	(1)	-----				
NP_004092_PAR3	(1)	-----	MKALIFAAAGLL	LLLPTFCQSGME	NDTNNLAKPTLP	IK
NP_005287_P2Y9	(1)	-----				
P79928_XP2Y	(1)	-----				
Consensus	(1)					
Section 2						
	(46)	46	60	70	80	90
AAH18130_PAR1L	(41)	-----	KVDGTS	SHVTGKG	VTVETVFSV	DE
NP_001983_PAR1	(46)	RNPNDKYEPFWE	DEEKNESGLTE	YRLVSINKSSP	LQKQLPAF	ISE
NP_835230_P2Y8	(1)	-----			MQVPNSTGPD	N
TransBD243560_HG52	(1)	-----			MQVPNSTGPD	N
NP_004092_PAR3	(39)	TFRGAPPNSFEE	FPFSALEGWTG	ATITVKIKCP	-EESASHLHV	KN
NP_005287_P2Y9	(1)	-----	MGDRRFIDFQ	FQDSNSSLRP	RGLGNATA	
P79928_XP2Y	(1)	-----	MTEDIMATSYP	TFLTTPYLP	MKELMNL	TNDT
Consensus	(46)				M V	D
Section 3						
	(91)	91	100	110	120	135
AAH18130_PAR1L	(64)	FSASVLTGKLT	TFVFLPIVY	TFIVFVGLPS	NGMALWVFL	FRTKKKKH
NP_001983_PAR1	(91)	DASGYLTSSWL	TFVPSVY	TGVEVVSLE	PLNIMAIIV	FILKMKVKK
NP_835230_P2Y8	(12)	ATLQMLRNPAI	AVALEP	VVYSLVAAVS	IEGNLFSLW	VLCRRMGPRS
TransBD243560_HG52	(12)	ATLQMLRNPAI	AVALEP	VVYSLVAAVS	IEGNLFSLW	VLCRRMGPRS
NP_004092_PAR3	(83)	ATMGYLTSSL	STKLIPATY	LLVFVVGVE	PANAVTLWM	LFFRTR-SI
NP_005287_P2Y9	(28)	NNTCTVDDSF	KYNLNGAV	YSVVEILGL	ITNSVSLF	VEFCFRMKMRS
P79928_XP2Y	(32)	EDTCVFDEG	FKFELLE	VPVSYSAVEM	VGLEPLNTA	AMWIEIAKMRPWN
Consensus	(91)	TL ML	V LPVVYSLV	FVVGLP	NIMALWVF	RMK R
Section 4						
	(136)	136	150	160	170	180
AAH18130_PAR1L	(109)	PAVTYMANLAL	ADLLSVIWF	PLKTA	YHIHGNNW	LYG
NP_001983_PAR1	(136)	PAVVYMLHLA	TADVLFMSV	LPFKIS	YFSGSDWQ	EGSEL
NP_835230_P2Y8	(57)	PSVIFMINLS	VTDLMLASV	LPFQIY	YHNCNRHH	WVEGVLL
TransBD243560_HG52	(57)	PSVIFMINLS	VTDLMLASV	LPFQIY	YHNCNRHH	WVEGVLL
NP_004092_PAR3	(127)	CTTVEYTNLA	IADFFECVT	LPEKIA	YHLNGNNW	VEGEVL
NP_005287_P2Y9	(73)	ETATFITNLA	VSDDLFEV	CTLP	EKIFYNFN	-RHWPEG
P79928_XP2Y	(77)	PTTVYMFNL	ALS	DTLYVLS	LPTLVY	YVADKNNW
Consensus	(136)	PTVIFM NL	AVADLLFV	LPFKIYYH	N W	VFGELLCKVVT

Section 5

	(181)	181	190	200	210	225
AAH18130_PAR1L (154)		FFYGNMYCSILFMTCLSVQRYWVI	VNPMGHSRKK-ANIAIGISLA			
NP_001983_PAR1 (181)		AFYCNMYASILLMTVISIDRFLAVVYPMQSLSWRTLGRASFTCLA				
NP_835230_P2Y8 (102)		AFYANMYSSILTMTCISVERFLGVLYPLSSKRWRRRRYAVAACAG				
TransBD243560_HG52 (102)		AFYANMYSSILTMTCISVERFLGVLYPLSSKRWRRRRYAVAACAG				
NP_004092_PAR3 (172)		IFYGNMYCSILLACISINRYLAIVHPFTYRGLPKHTYALVTCGL				
NP_005287_P2Y9 (117)		AFLTNIYGSMLFLTCTISVDRFLAIVYPFRSRTITRTRNSAIVCAG				
P79928_XP2Y (122)		LFYANLYSSILFLTCTISVHRYRGVCHPITSLRMRNAKHAYVICAL				
Consensus (181)		AFYANMYSSIL MTCISVDRFLAVVYPLSSKR R RYAV CAG				

Section 6

	(226)	226	240	250	260	270
AAH18130_PAR1L (198)		TWLLTLLVTIPLYVVKQTI	FIPALNITTC	HDVLEPEQLL	--VGDMF	
NP_001983_PAR1 (226)		EWALAIAGVVPVLKEQTIQVPGENITTC	HDVLENETLL	--EGYYA		
NP_835230_P2Y8 (147)		TWLLLTALSPARTDLTYPVHALGITTC	FDVLKWTMLPSVAMWA			
TransBD243560_HG52 (147)		TWLLLTALSPARTDLTYPVHALGITTC	FDVLKWTMLPSVAMWA			
NP_004092_PAR3 (217)		VWATVFLYMLFFFILKQEYYLVQPDITTC	HDVHNTCES--SSPFQL			
NP_005287_P2Y9 (162)		VWILVLSGGISASLFTSTNVNNT--TTC	FEFGSKRVW--KTYLS			
P79928_XP2Y (167)		VWLSVTLCLEVNLI	IFVTVSPKVKN--TIC	HDTRPEDF--ARYV		
Consensus (226)		VWLLVL ALIPL I T V AL ITTCHDVL LL A WA				

Section 7

	(271)	271	280	290	300	315
AAH18130_PAR1L (241)		NYFLSLATGVTFFPAFLTASAYVLMTRMIRS	SAMDENS---	EKKR		
NP_001983_PAR1 (269)		YFSAFSAVFFVPLTIISTVCYVSIIRCLSSSAVANRS---	KKS			
NP_835230_P2Y8 (192)		VFLFTIFILLFLIPFVITVACYTATILKLLRTEEAHGR---	EQRR			
TransBD243560_HG52 (192)		VFLFTIFILLFLIPFVITVACYTATILKLLRTEEAHGR---	EQRR			
NP_004092_PAR3 (261)		YFISLAFGGFLIPFVLTITYCYAATRTLN---	AYDHR--WLWY			
NP_005287_P2Y9 (203)		KITIFIEVVGFIIPLIILNVSCSSVVLRTLRK	PATLSQI--GTNK			
P79928_XP2Y (207)		EYSTAIMCLLFGITPCLTIAGCYGLMTRLMKPIVSGNQOTLPSYK				
Consensus (271)		Y SI ILLFLIP VITVACY AIIR L KS A R				

Section 8

	(316)	316	330	340	350	360
AAH18130_PAR1L (283)		KRAIKLIVSVLAMYLTCTPSNLLLVVHYFLIKSQGQ----	SHV			
NP_001983_PAR1 (311)		--ALFLSAAVFCIFLIICFPTNVLEIAHYSFLSHTST----	TEAA			
NP_835230_P2Y8 (234)		-RAVGLAAAVVLTAEVTCFAPNNFVLLAHIVSR	LFYG-----KSY			
TransBD243560_HG52 (234)		-RAVGLAAAVVLTAEVTCFAPNNFVLLAHIVSR	LFYG-----KSY			
NP_004092_PAR3 (300)		---VKASLLILVIFTICFAPSNIILIIHHANYYYNN----	TDGL			
NP_005287_P2Y9 (245)		KKVLKMITVHMAVEVVCVFPYNSVFLYALVRSQAITNCFLE	RFA			
P79928_XP2Y (252)		KRSIKTIIFVMTAFALCFMPFHTITRTLYYYARLLGIK-CYALNVI				
Consensus (316)		RAVKLA VLLIFVICFAP NIVLILHY R				

Section 9

	(361)	361	370	380	390	405
AAH18130_PAR1L (323)		YALYI	VALCLSTLNS	CIDPFVYYFVSHDE	RDHAKNAL	LCRSVR--
NP_001983_PAR1 (350)		YFAYLL	CVCVSSISS	CIDPLIYYFAS	SECORYVYSIL	CCKESSD-
NP_835230_P2Y8 (272)		YHVKLT	TLCLSLNNCL	DPFVYFASRE	FQLRLREYL	GCRRVPR-
TransBD243560_HG52 (272)		YHVKLT	TLCLSLNNCL	DPFVYFASRE	FQLRLREYL	GCRRVPR-
NP_004092_PAR3 (337)		YFIYLI	ALCLGSLNS	CIDPFLYFLM	SKTRNHSTAY	LTK-----
NP_005287_P2Y9 (290)		KIMYPIT	LCLATLNC	CFDPFIYYFT	LESFQKSFYI	NAHIRMESL-
P79928_XP2Y (296)		NVTYKV	TRPLASANS	CIDPILYEL	ANDRYRRRL	IIRTVRRSSVPN
Consensus (361)		Y VY	LTLCLSSLNS	CIDPFVYYFAS	EFQ L	L CR

Section 10

	(406)	406	420	430	440	450
AAH18130_PAR1L (366)		----	TVKQMQVSLT	SKKHSRKS	SSYSSSSTTV	KTSY-----
NP_001983_PAR1 (394)		----	PSSYNSSGQL	MASKMDTCSS	NLNNSIYK	LLT-----
NP_835230_P2Y8 (316)		----	DTLDTTRRES	SLFSARTTS	SVRSEAGAH	PEGMEGATRPGLQRQE
TransBD243560_HG52 (316)		----	DTLDTTRRES	SLFSARTTS	SVRSEAGAH	PEGMEGATRPGLQRQE
NP_004092_PAR3 (375)		----	----	----	----	----
NP_005287_P2Y9 (334)		----	FKTETPLT	TKPSLP	AIQEEVSDQ	TNNGGELMLESTF----
P79928_XP2Y (341)		RRCMH	TINHPQTE	PHMTAGPL	PVISC	AEEIPSNCSMVRDENGEGSRE
Consensus (406)			T	SL SAK	S	G

Section 11

	(451)	451	460	470	480	495
AAH18130_PAR1L (398)		-----	-----	-----	-----	-----
NP_001983_PAR1 (426)		-----	-----	-----	-----	-----
NP_835230_P2Y8 (357)		SVF-----	-----	-----	-----	-----
TransBD243560_HG52 (357)		SVF-----	-----	-----	-----	-----
NP_004092_PAR3 (375)		-----	-----	-----	-----	-----
NP_005287_P2Y9 (371)		-----	-----	-----	-----	-----
P79928_XP2Y (386)		HRVEWTD	TKEINQMMN	RRSTIKRN	STDKNDM	KENRHGENYLPYVE
Consensus (451)						

Section 12

	(496)	496	510	520	530	540
AAH18130_PAR1L (398)		-----	-----	-----	-----	-----
NP_001983_PAR1 (426)		-----	-----	-----	-----	-----
NP_835230_P2Y8 (360)		-----	-----	-----	-----	-----
TransBD243560_HG52 (360)		-----	-----	-----	-----	-----
NP_004092_PAR3 (375)		-----	-----	-----	-----	-----
NP_005287_P2Y9 (371)		-----	-----	-----	-----	-----
P79928_XP2Y (431)		VVEKEDY	ETKREN	KTTEQSS	KTNAEQDEL	QTQIDSRLKRGKWQL
Consensus (496)						

Section 13

	(541)	541	550	560	570	585
AAH18130_PAR1L (398)	-	-	-	-	-	-
NP_001983_PAR1 (426)	-	-	-	-	-	-
NP_835230_P2Y8 (360)	-	-	-	-	-	-
TransBD243560_HG52 (360)	-	-	-	-	-	-
NP_004092_PAR3 (375)	-	-	-	-	-	-
NP_005287_P2Y9 (371)	-	-	-	-	-	-
P79928_XP2Y (476)	S	S	K	K	G	A
Consensus (541)						

Section 14

	(586)	586	602
AAH18130_PAR1L (398)	-	-	-
NP_001983_PAR1 (426)	-	-	-
NP_835230_P2Y8 (360)	-	-	-
TransBD243560_HG52 (360)	-	-	-
NP_004092_PAR3 (375)	-	-	-
NP_005287_P2Y9 (371)	-	-	-
P79928_XP2Y (521)	E	E	V
Consensus (586)			